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Amino Acid Sequence of hPygo2

MAASAPPPDKLEGGGGPAPPPAPPSTGRKQGKAGLQMKSP**EKK**
RRKSNTQGPAYSHLTEFAPPPTPMVDHLVASNPFEDDFGAPKVG
VAAPPFLGSPVPFGGFRVQGGMAGQVPPGYSTGGGGGPQPLRRQ
PPPFPPNPMGPAFNMPPQGGPYPPPGNMNFPSQPFNQPLGQNFS
PPSGQMMPGPVGGFGPMISPTMGQPPRAELGPPSLSQRFAQPGA
PFGPSPLQRPGQGLPSLPPNTSPFPGPDGFPGPGGEDGGKPLN
PPASTAFPQEPHSGSPAAAVNGNQPSFPPNSSGRGGGTPDANSL
APPGKAGGGSGPQPPPGLVYP**CGACRSEVNDDQDAILCEASCOK**
WFHRECTGMTESAYGLLTTEASAVWACDLCLKTKEIQSVYIREGM
GQLVAANDG

FIG. 1

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ALIGNMENT OF HPYGO1 VS HPYGO2

VERSION BLASTP 2.2.6

Sequence 1 gi 19550449 pygopus 1 [Homo sapiens] Length 419 (1 .. 419)
 Sequence 2 gi 21594198 Pygopus 2 [Homo sapiens] Length 406 (1 .. 406)

Score = 240 bits (613)

Identities = 161/439 (36%)

Positives = 214/439 (48%)

Gaps = 58/439 (13%)

```

Pygo1: 3  AENSPAPAYKVSSHGGDSGLDG-----LGGPGVQLGSPDKKKRKANTQGSPFPPLSEY 55
      A ++P P K+  GG +                      G G+Q+ SP+KK+RK+NTQGP++ L+E+
Pygo2: 2  AASAPPPPKLEGGGGPAPPPAPPSTGRKQKGAGLQMKSPKKRRKSNTQGPAYSHLTF 61

Pygo1: 56  APPPNPNSDHLVAANPFDDNYNTISYKPLPSSNPYLGPYPGGGYSTFR-MPPHVPPRM 114
      APPP P DHLVA+NPF+D++  + K  ++ P+LG  P FGG+      M  VPP
Pygo2: 62  APPPTPMVDHLVASNPFEDDFG--APKVGVAAPPFLGSPVP-FGGFRVQGGMAGQVPPGY 118

Pygo1: 115 SSPYCG-PYSLRNQPHFPFQNPPLGMGFNRP-HAFNFGPHDNSSFGNPSYNNALSQNVNMP 172
      S+  G P LR QP PFP NP+G FN P      + P N +F +  +N L QN + P
Pygo2: 119 STGGGGGPQPLRRQPPPPFPNPMGPAFNMPPQGGPYPPPGNMNFPSQPFNQPLGQNFSP 178

Pygo1: 173 NQHFRQNPANFNSQI-----PPQNASQVSNPDLASNFVPGNNSNFTSPLESNHSFIP- 224
      +      P  F  +      PP+  +++  P L+  F      SPL+      +P
Pygo2: 179 SGQMMPGPGVGGFGPMISPTMGQPPR--AELGPPSLSORFAQPGAPFGPSPQLRPGQGLPS 236

Pygo1: 225 -PPNTFGQAKAPPPKQDFTQGATKNTNQNSSAHPPHLNMDDTVNQSNIELKNVNRNNAVN 283
      PPNT      +P P D      +      +PP      + A
Pygo2: 237 LPPNT-----SPFPGPDGFPGPGGEDGGKPLNPP-----ASTAFP 272

Pygo1: 284 QENSRSSTTEATNNNPANGTQNKPRQPRGAADACTTEKSNKSSLHPNRRHGHSSSDP---- 339
      QE  S  A N N +  N + G DA +      K+      G S  P
Pygo2: 273 QEPHSGSPAAAVNGNQPSFPPNSSGRGGGTPDANSLAPPGKAG-----GGSGPQPPPG 326

Pygo1: 340 VYPCGICTNEVNDDQDAILCEASCQKWFHRICTGMTETAYGLLTAEASAVWGCDTCMADK 399
      VYPCG C +EVNDDQDAILCEASCQKWFHR CTGMTE+AYGLLT AEASAVW CD C+  K
Pygo2: 327 VYPCGACRSEVNDDQDAILCEASCQKWFHRECTGMTESAYGLLTTEASAVWACDLCLKTK 386

PHD-finger.
PHD folds into an i>
330 *****
Pygo1: 400 DVQLMRTRETFGPSAVGSD 418
      ++Q + RE G      +D
Pygo2: 387 EIQSVYIREGMGQLVAAND 405

```

FIG. 2

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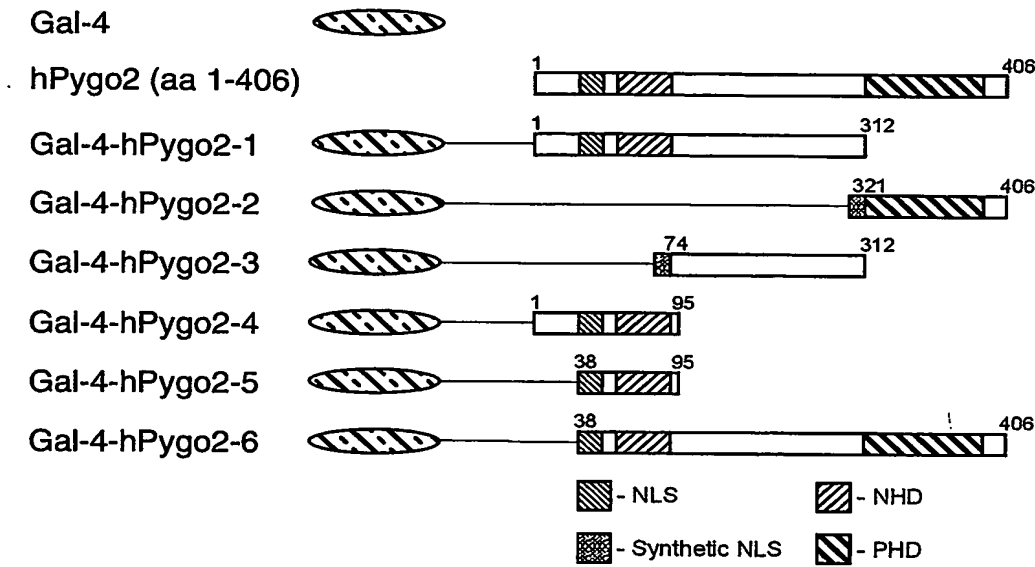


FIG. 3A

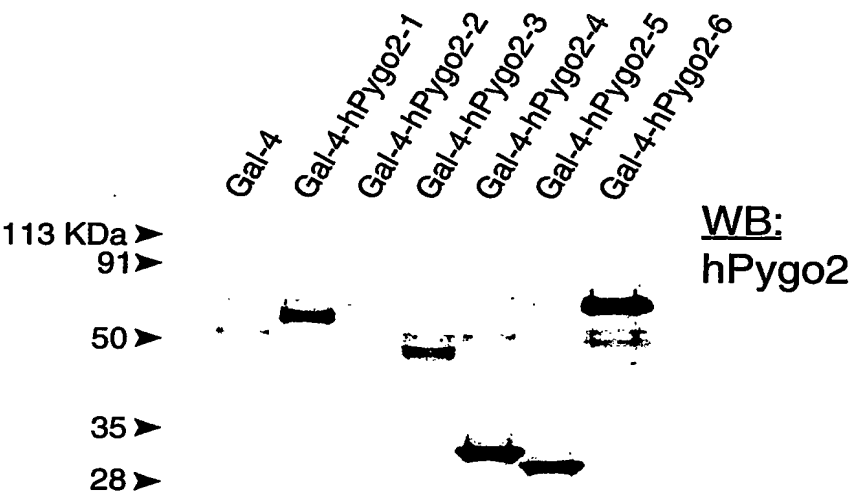


FIG. 3B

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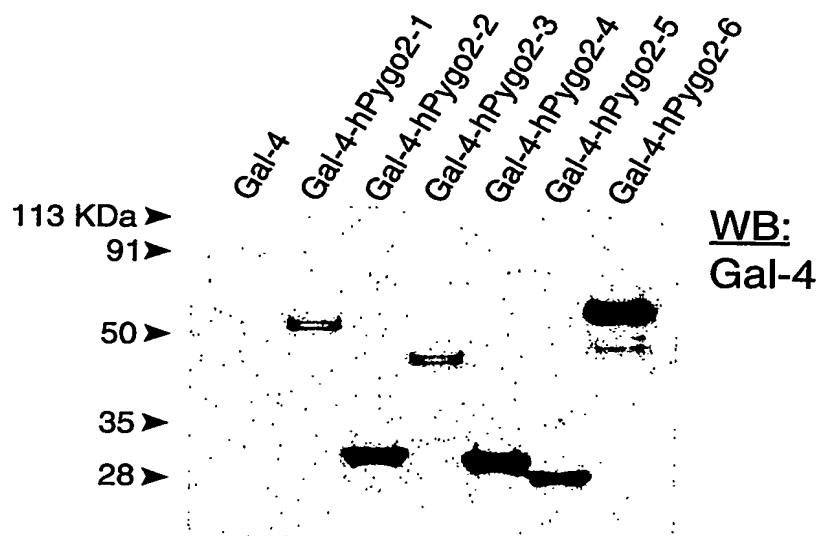


FIG. 3C

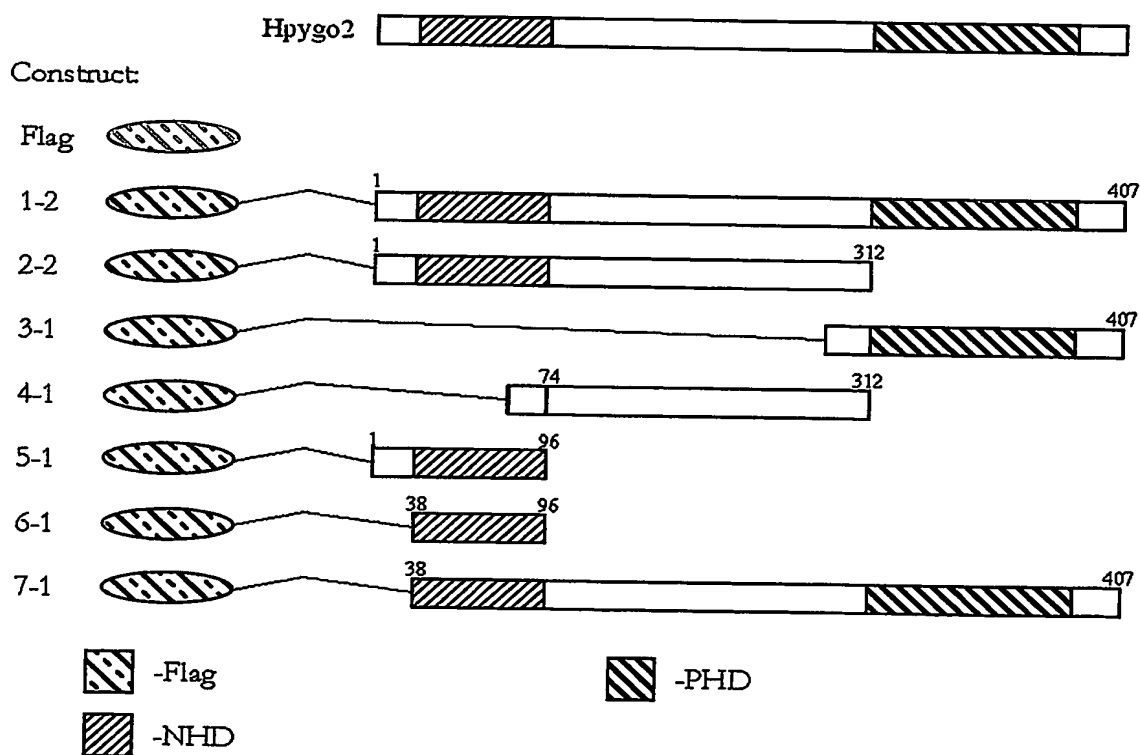
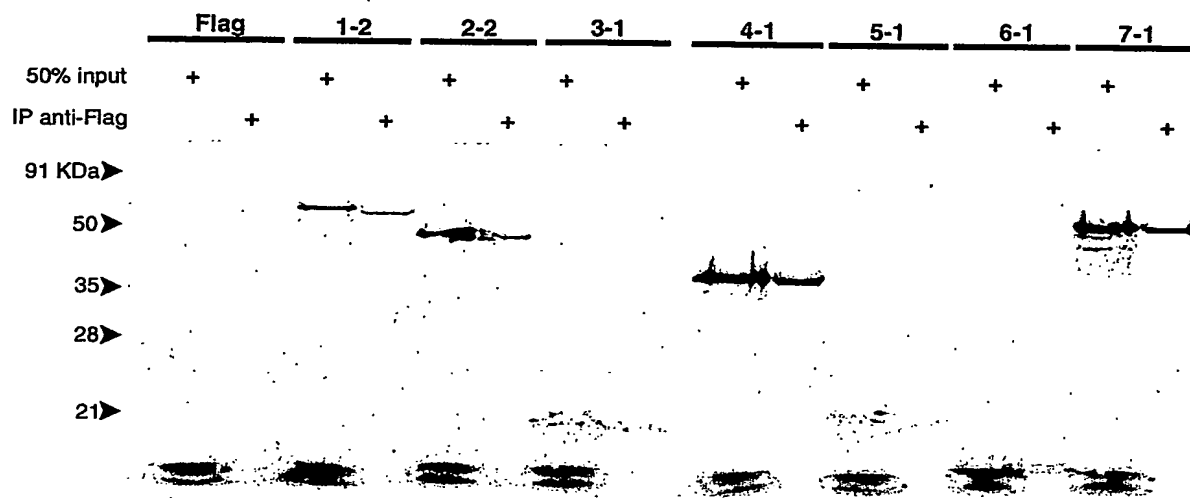
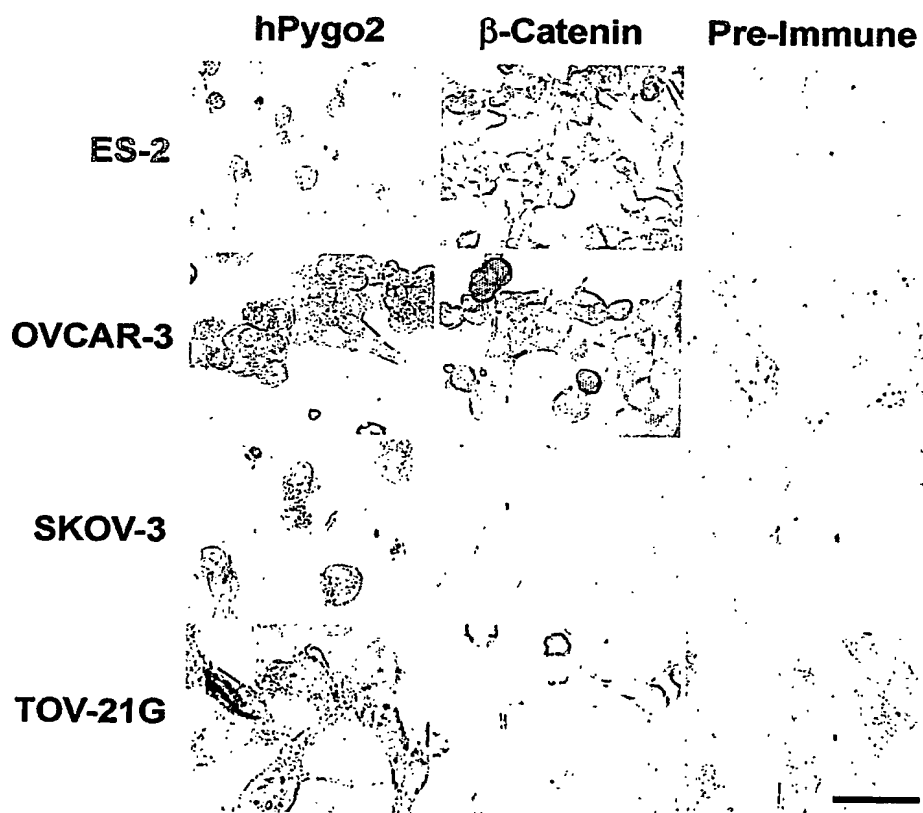


FIG. 3D

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**FIG. 3E****FIG. 3F**

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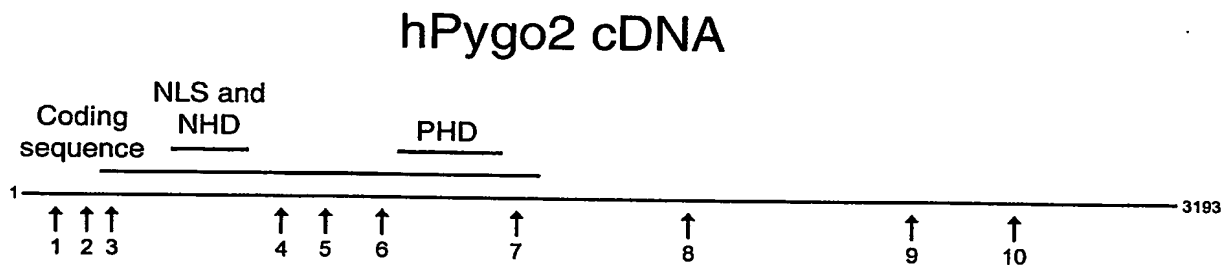


FIG. 3G

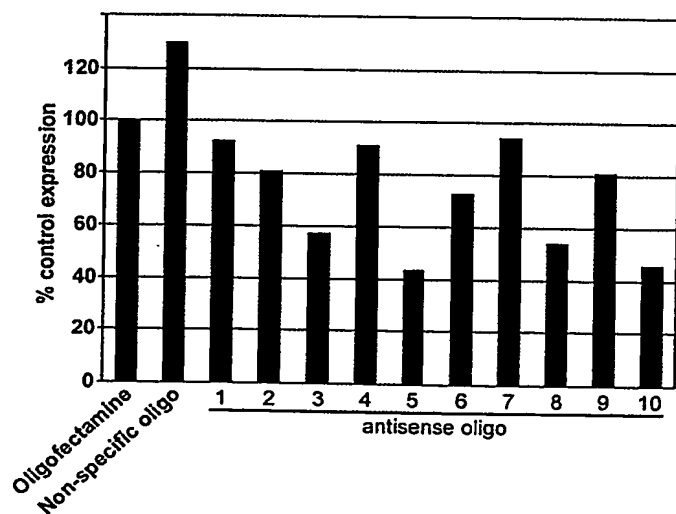
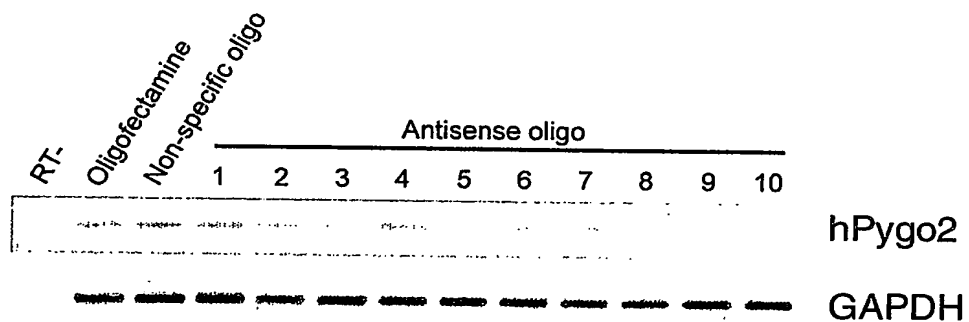


FIG. 3H

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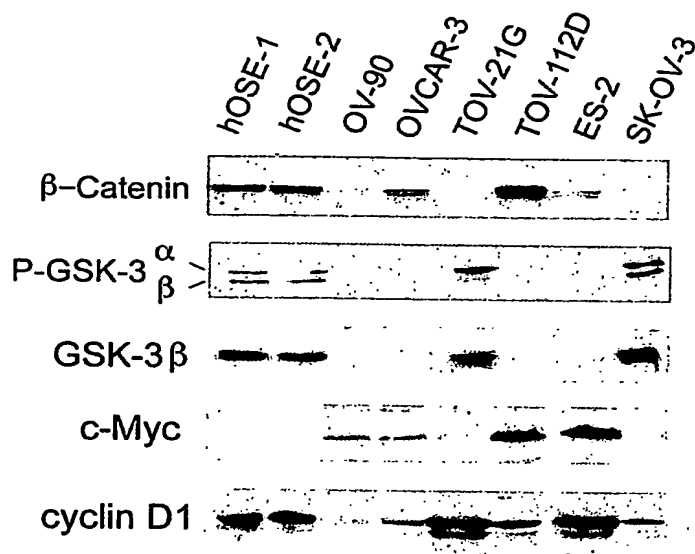


FIG. 4A

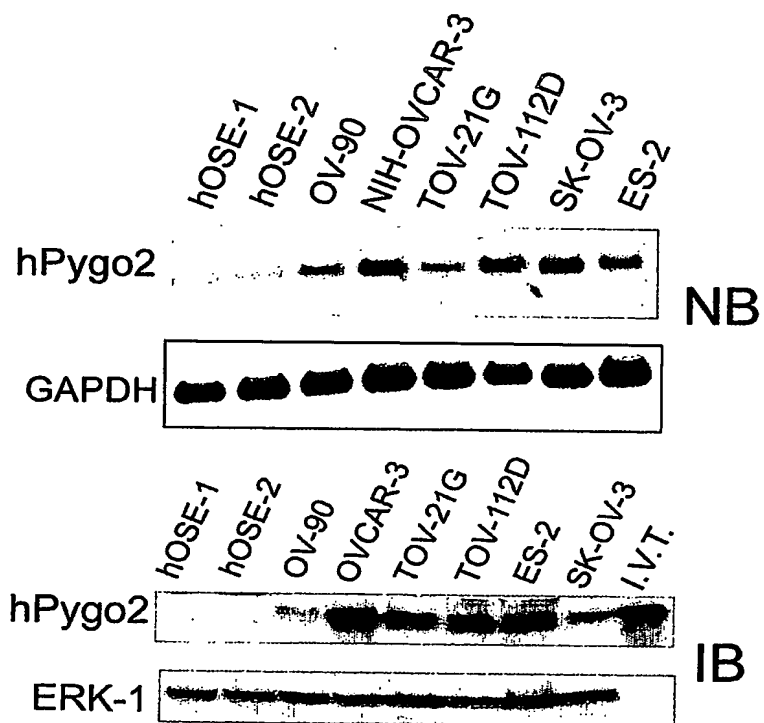


FIG. 4B

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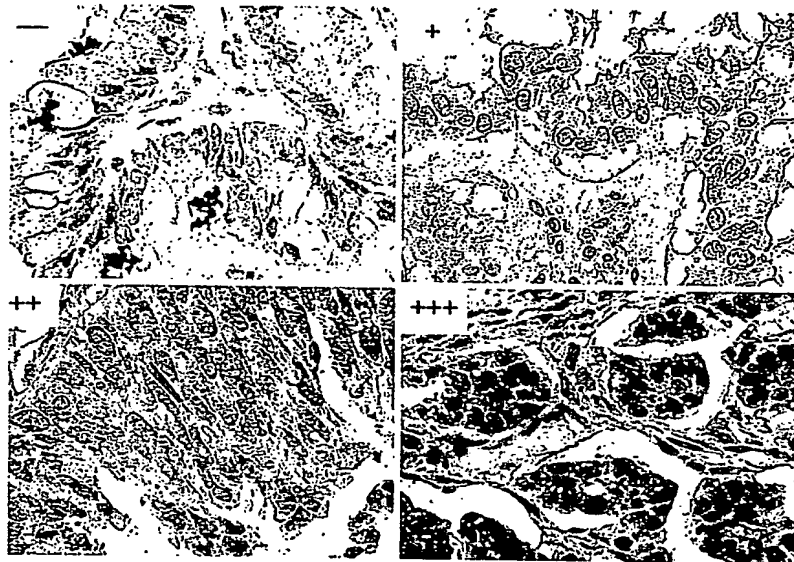


FIG. 4C

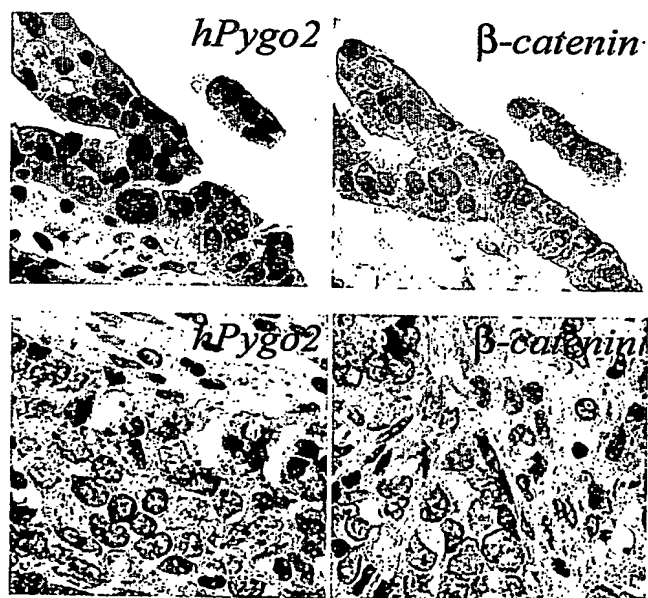


FIG. 4D

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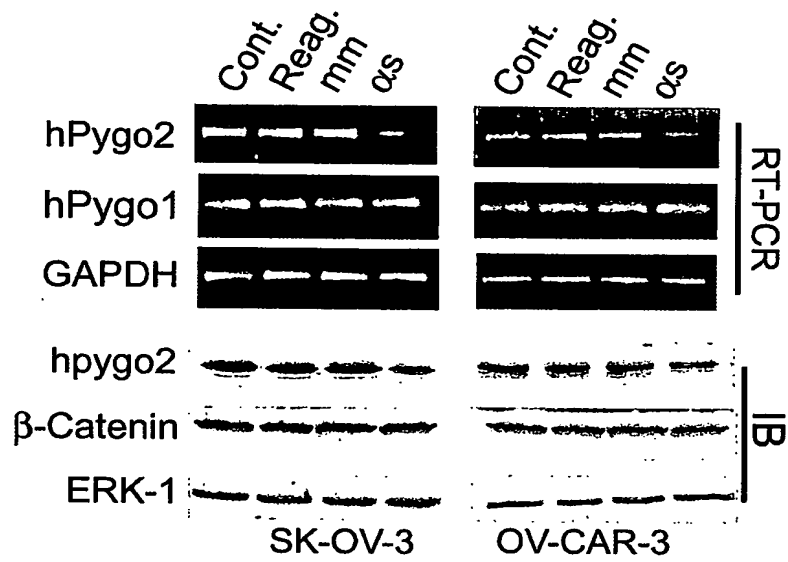


FIG. 5A

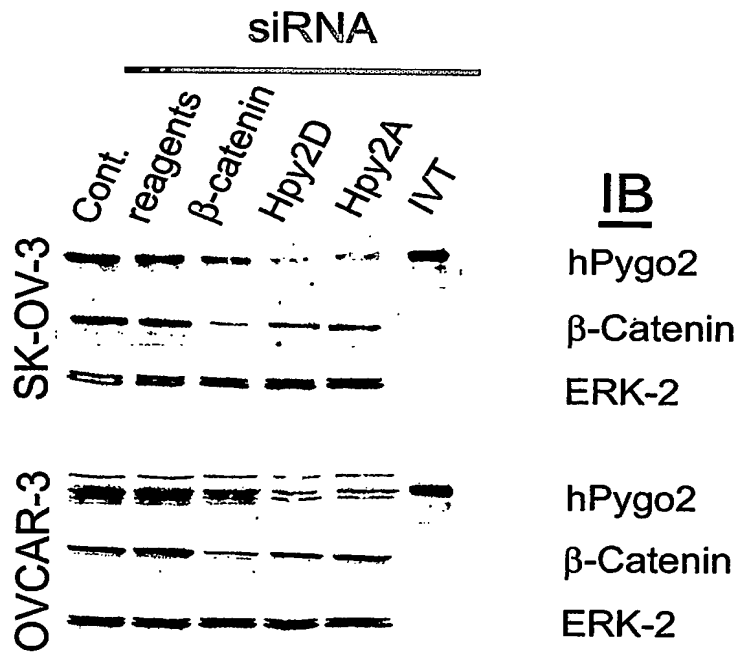
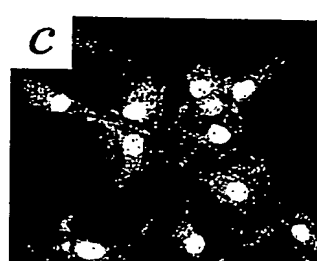
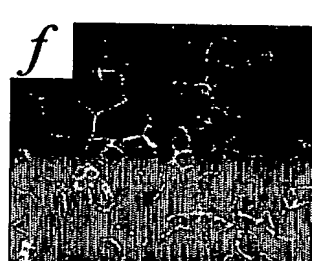
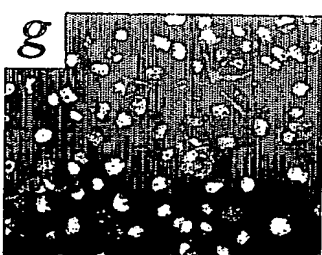
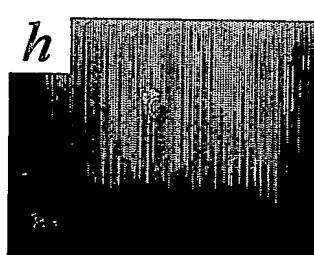
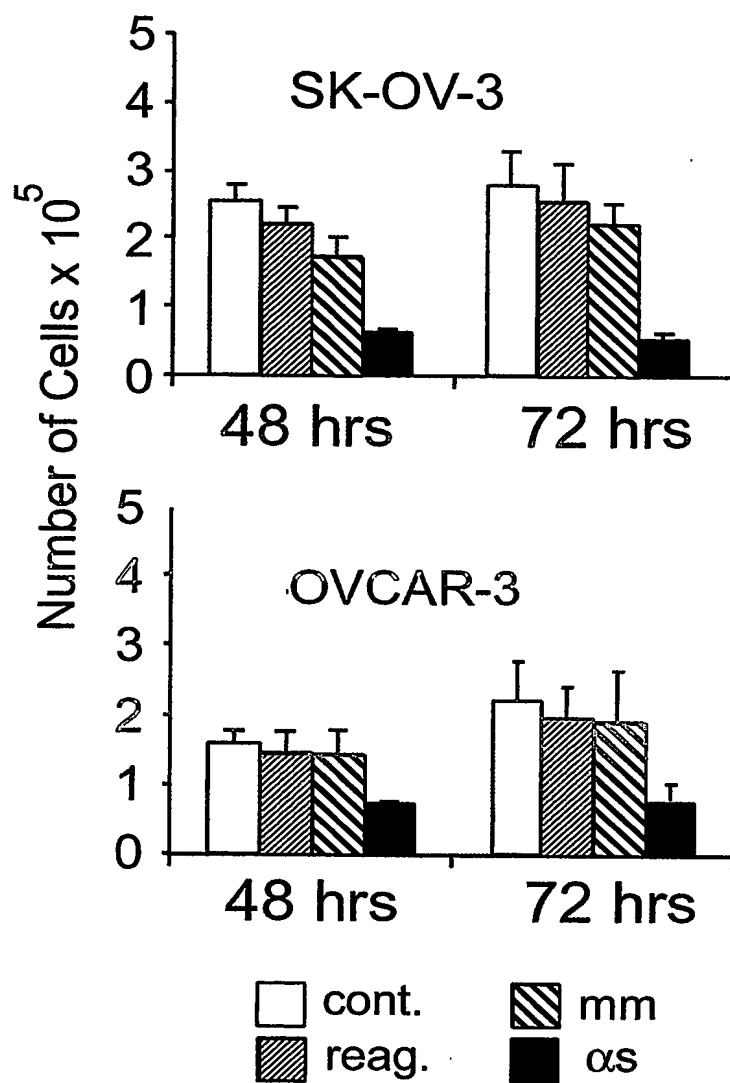


FIG. 5B

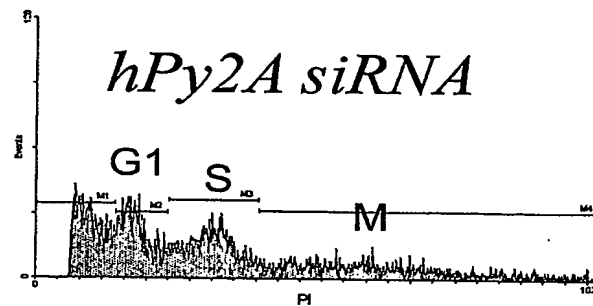
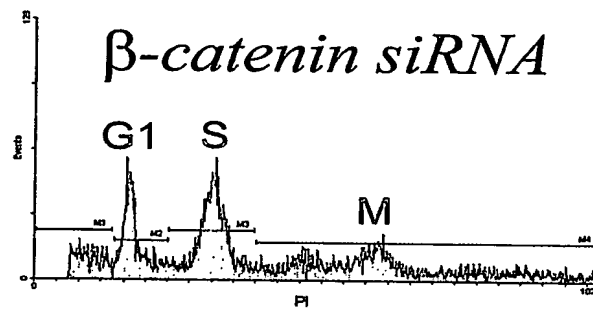
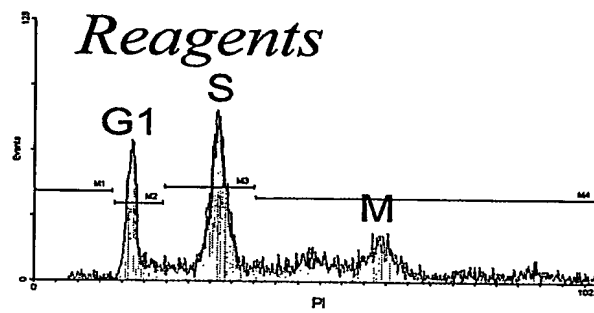
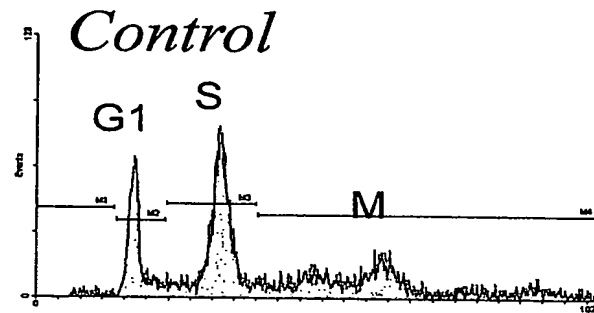
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**FIG. 6A****FIG. 6B****FIG. 6C****FIG. 6D****FIG. 6E****FIG. 6F****FIG. 6G****FIG. 6H****FIG. 6I****FIG. 6J****FIG. 6K****FIG. 6L**

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**FIG. 7A**

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**FIG. 7B**

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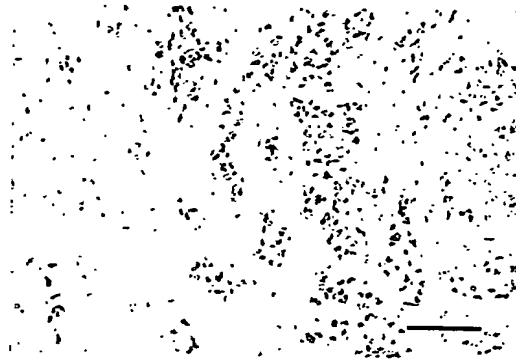


FIG. 8A

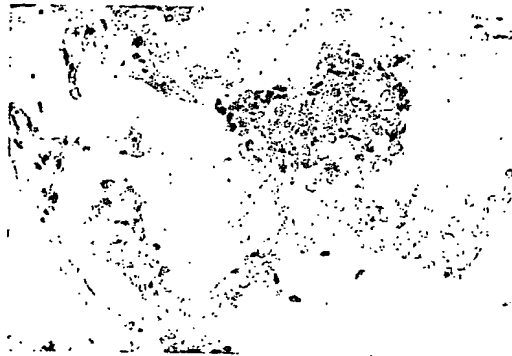


FIG. 8B

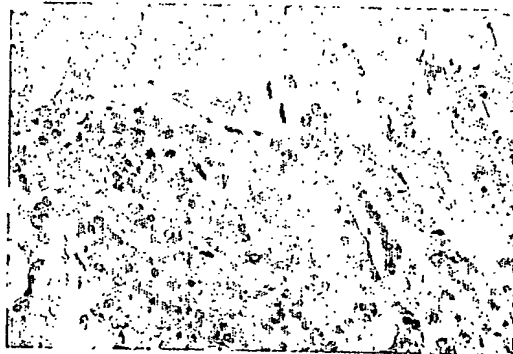


FIG. 8C

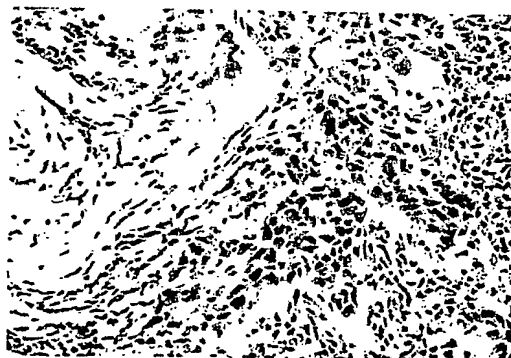


FIG. 8D

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FIG. 9A

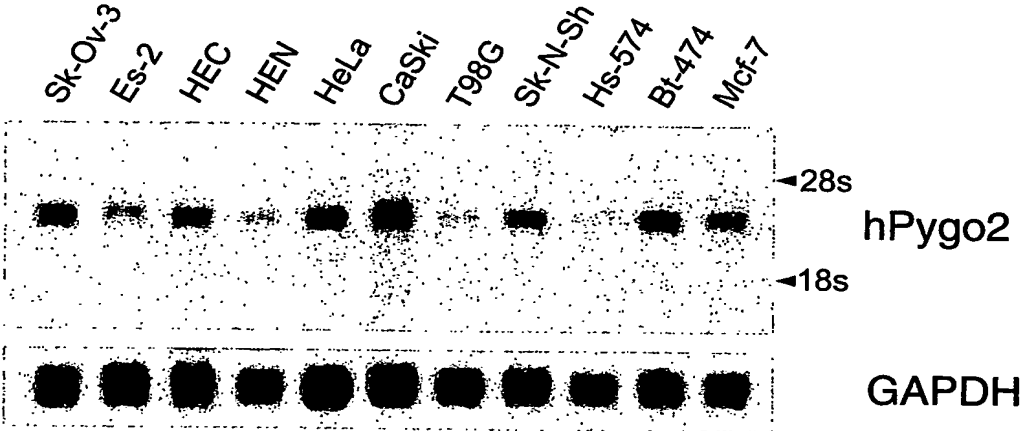


FIG. 9B

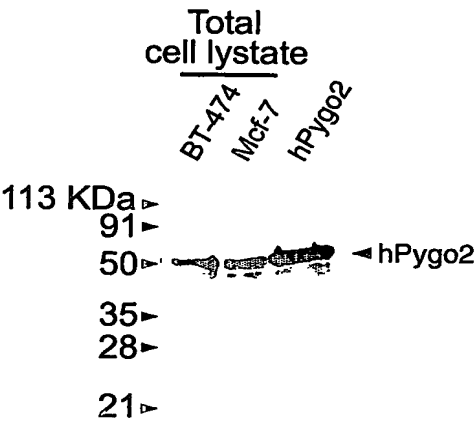


FIG. 9C

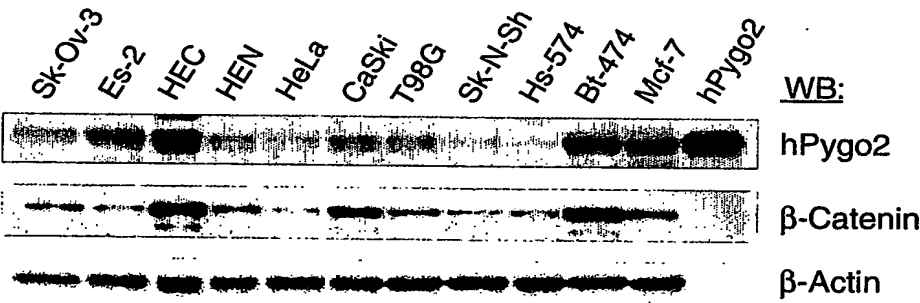
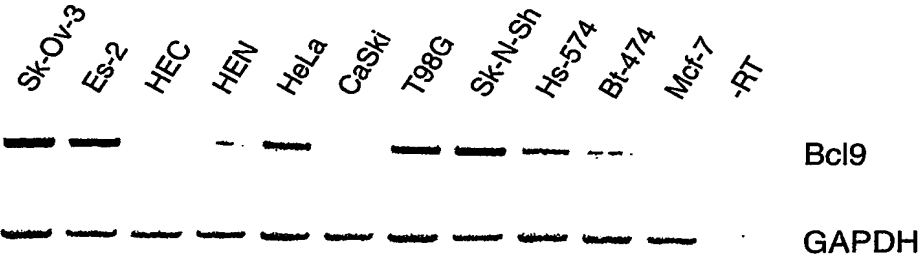


FIG. 9D



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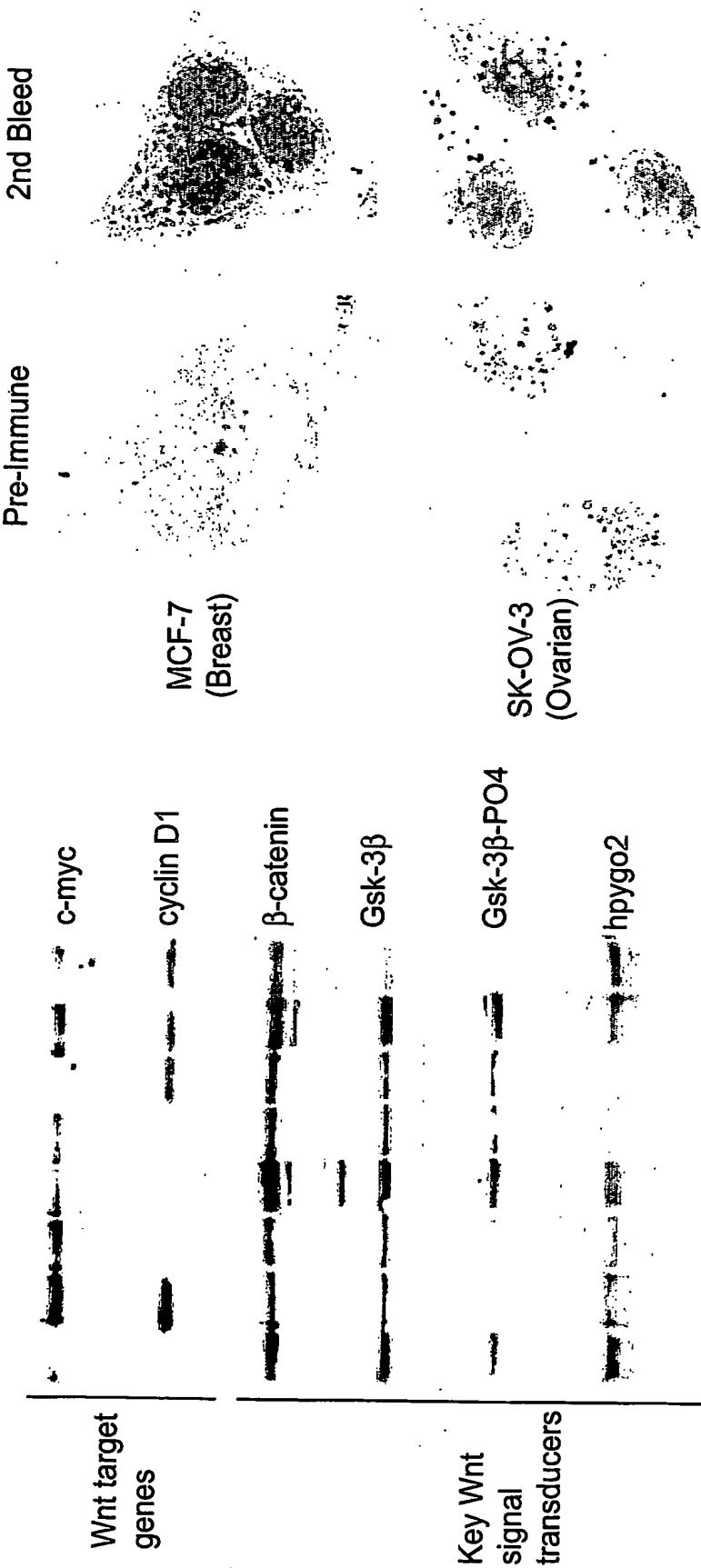


FIG. 9F

FIG. 9E

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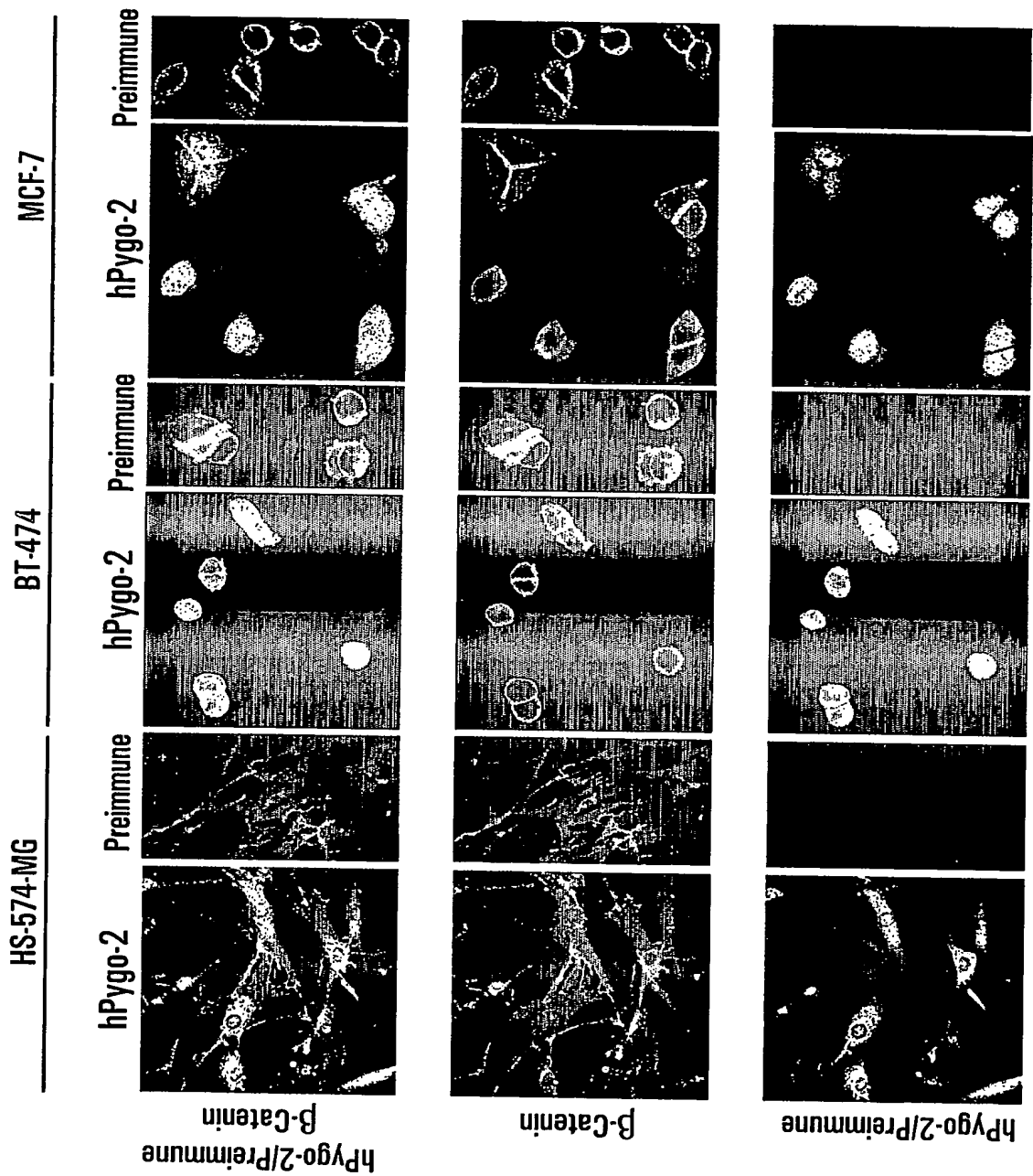
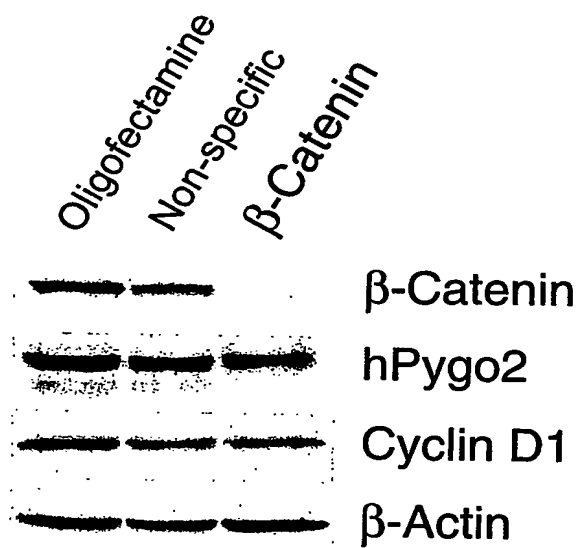
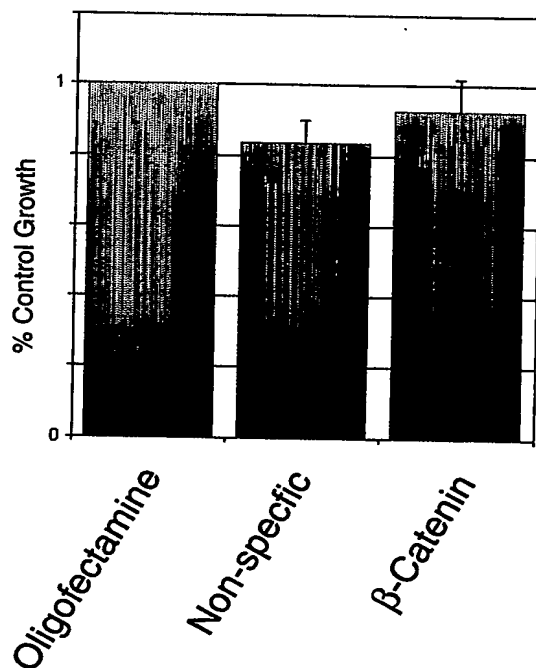


FIG. 10

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**FIG. 11A****FIG. 11B**

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FIG. 12A

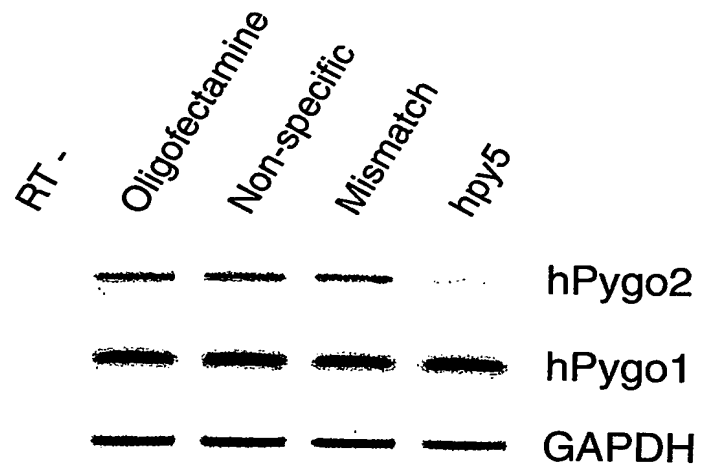
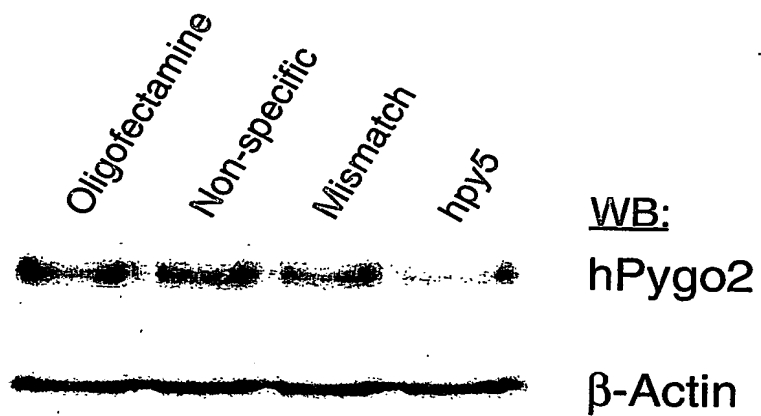
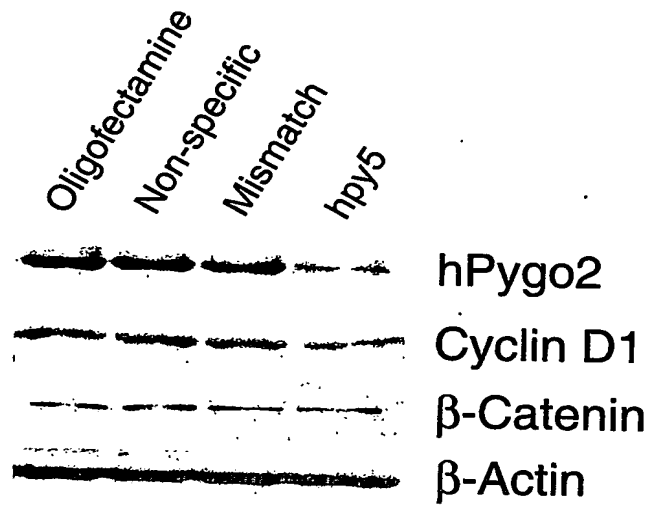
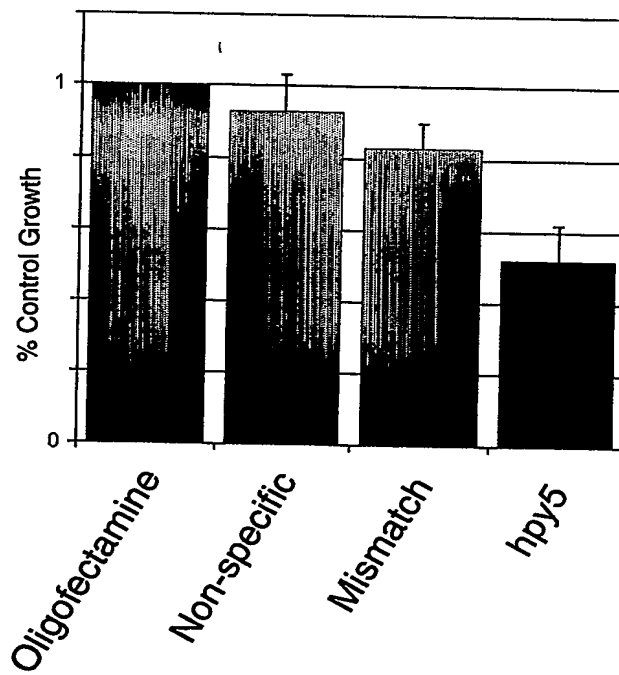


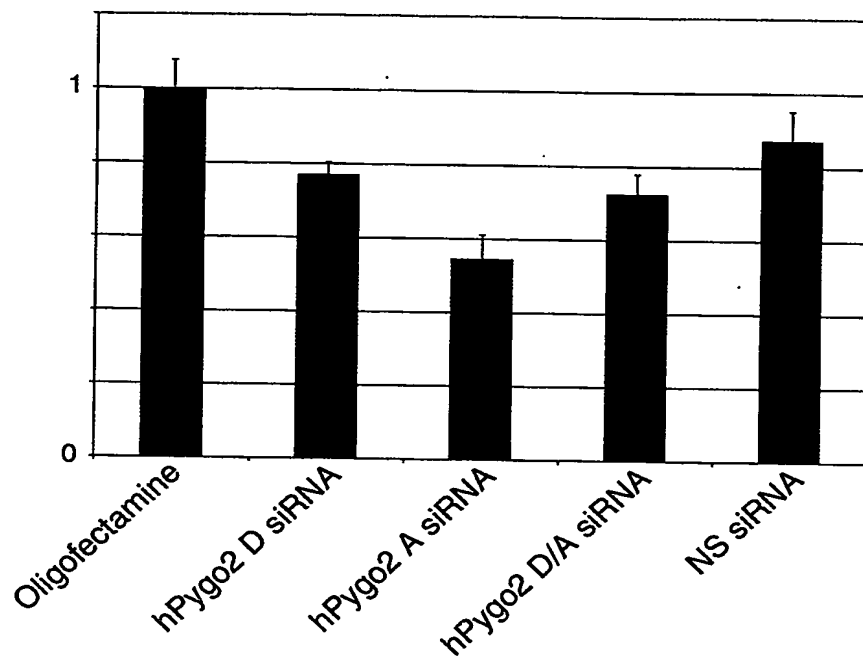
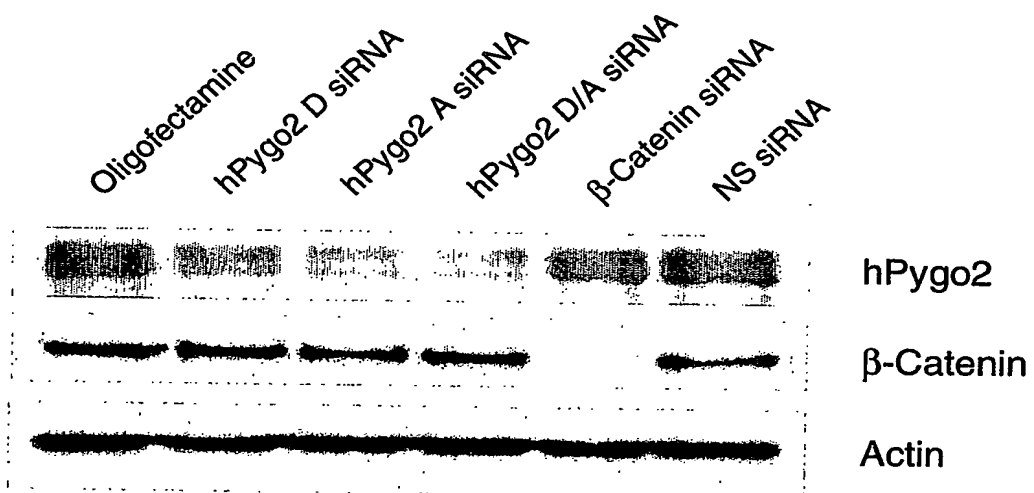
FIG. 12B



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FIG. 13A**FIG. 13B**

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**FIG. 14A****FIG. 14B**

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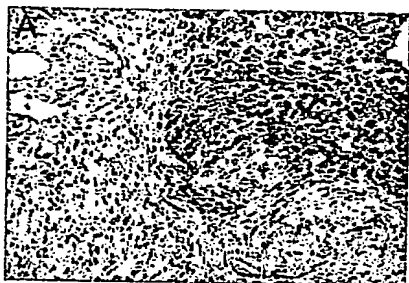


FIG. 15A



FIG. 15B

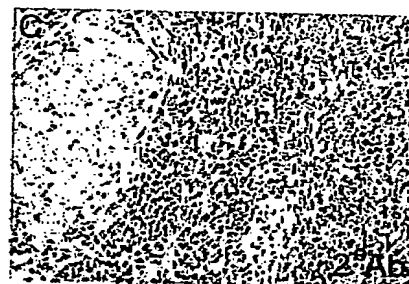


FIG. 15C



FIG. 15D

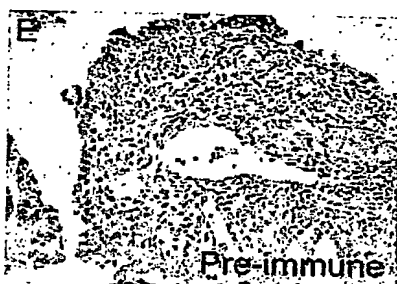


FIG. 15E



FIG. 15F

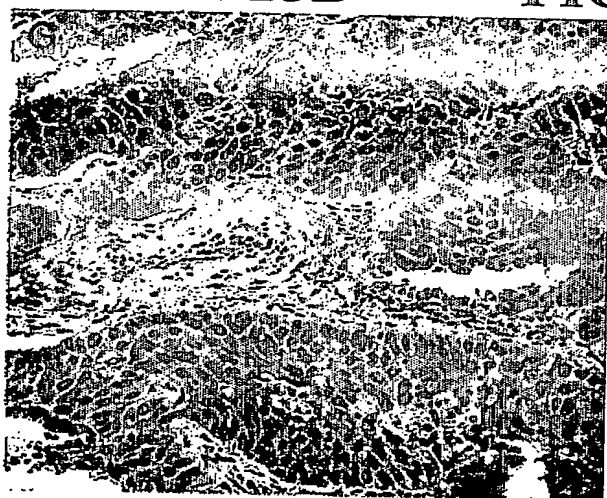


FIG. 15G

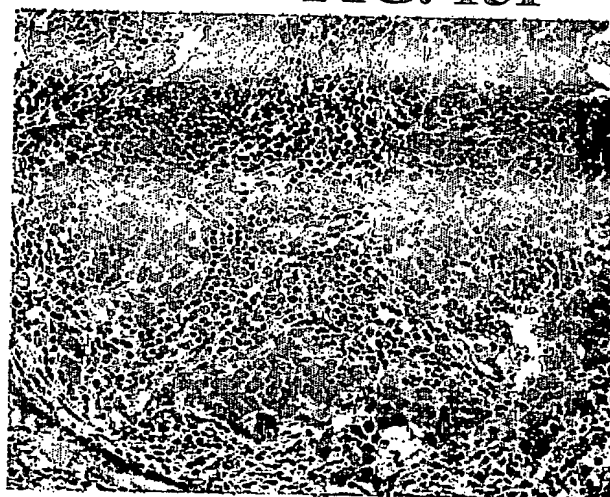


FIG. 15H

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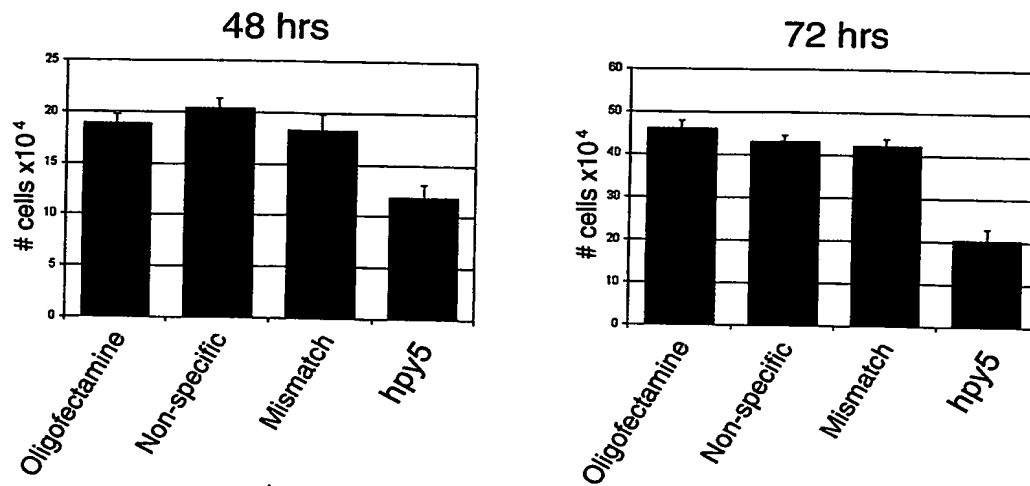


FIG. 16A

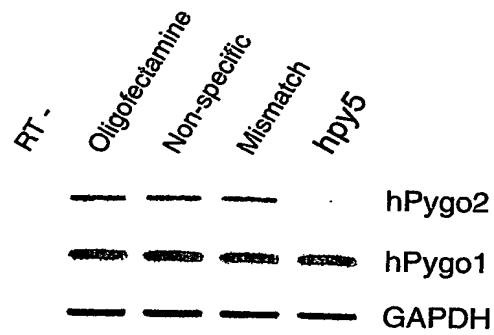


FIG. 16B

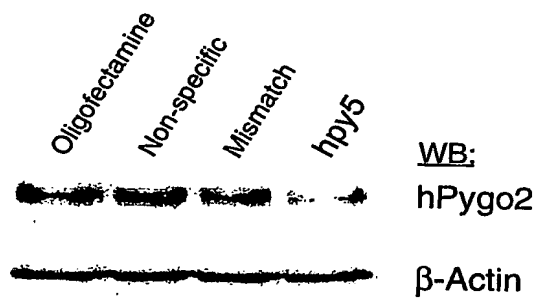


FIG. 16C